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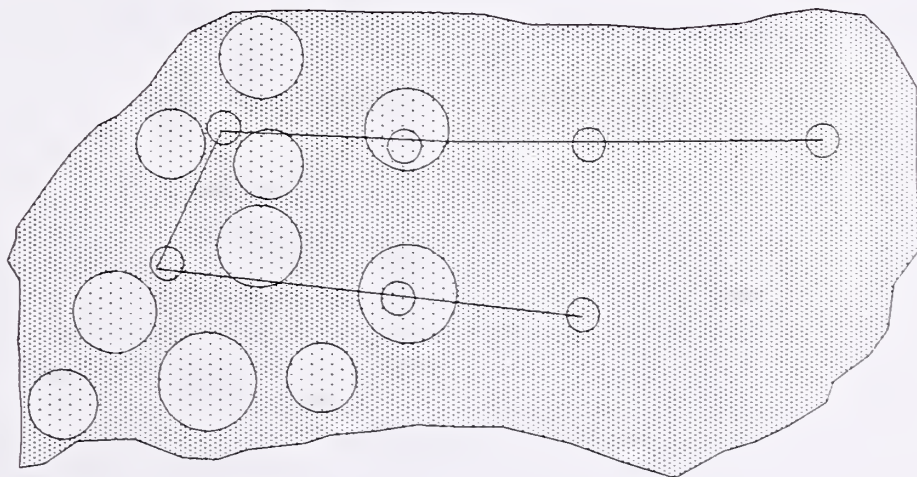
Fort Collins,
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Research Paper
RM-303



Sensitivity of the Western Root Disease Model: Inventory of Root Disease

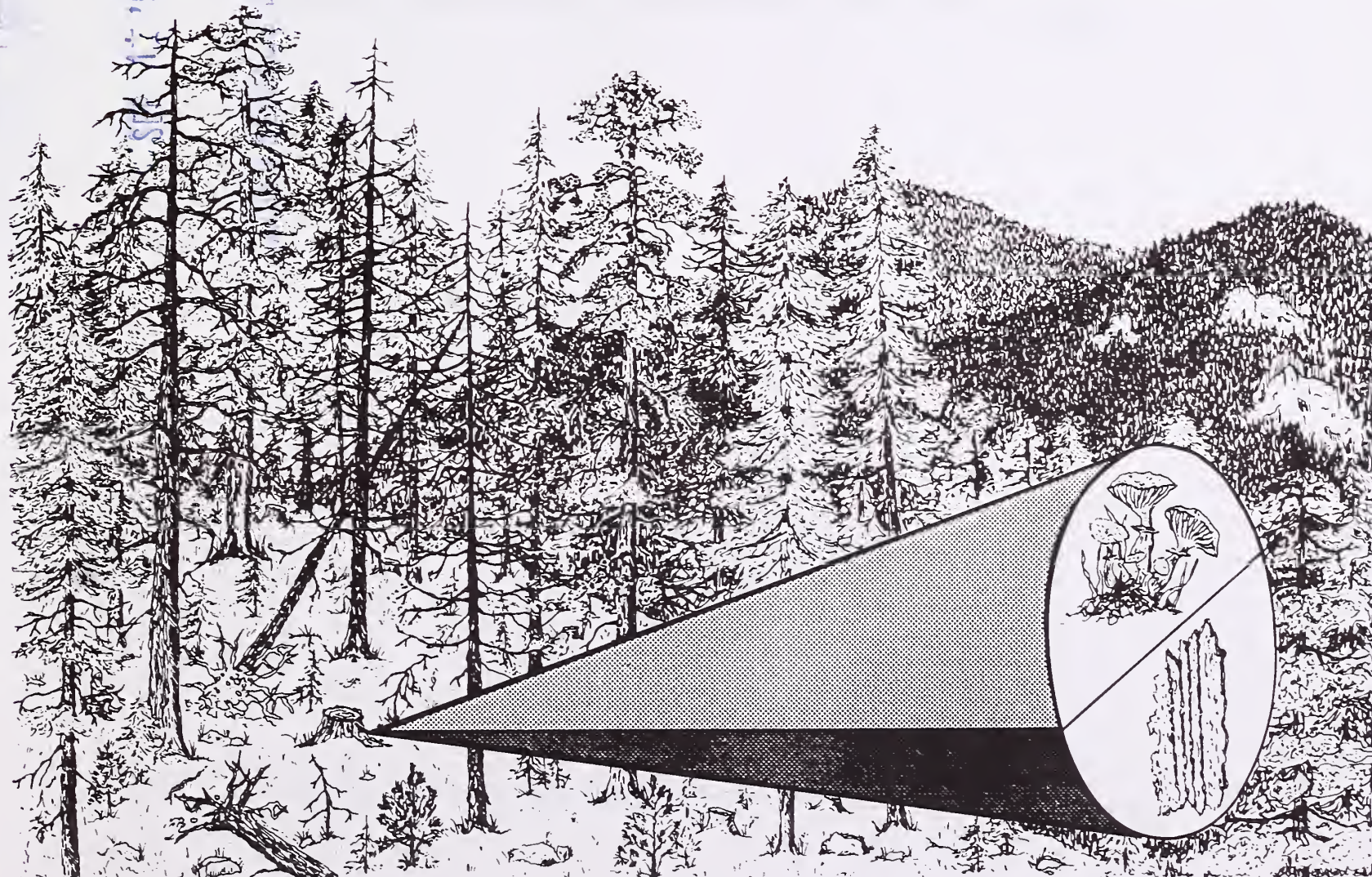
Michael A. Marsden



ROOT ROT CENTERS



INVENTORY PLOTS



Abstract

The Western Root Disease Model can be used to simulate the spread and impact of *Armillaria* spp. and *Phellinus weirii* (Murr.[Gilbn.]) in western coniferous forests. The simulations are sensitive to the information on initial disease conditions supplied to the model. This includes the number, size, and location of root disease centers. The model has limited capacity to simulate the spatial pattern of root disease centers. When the disease is scattered throughout the stand, it can be simulated as a single, large center. Forest inventory requirements and model limitations are demonstrated.

Keywords: *Armillaria*, *Phellinus weirii*, Prognosis Model, disease impact

Sensitivity of the Western Root Disease Model: Inventory of Root Disease

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Sensitivity of the Western Root Disease Model: Inventory of Root Disease

Michael A. Marsden

Introduction

The Western Root Disease Model was recently developed to model the spread and impact of *Armillaria* spp. and *Phellinus weirii* (Murr.[Gilbn.]) in western coniferous forests. The basic model design and user options are described in the *User's Manual for Western Root Disease Model* (Stage et al. 1990). A sensitivity analysis of the user input parameters provides the user with some guidelines to the importance of the starting parameters for the model.²

The considerations needed for data on location of root disease centers within the stand are addressed here. Information on the location of disease centers within the stand must be supplied to the model. However, the model has limited ability to represent the spatial attributes of the stand. Default values for the number of centers, total area infected, proportion of trees infected, and the location of centers will be used in the absence of user-specific values (Stage et al. 1990).

The data the user supplies on root disease conditions in a stand can be divided into two types: 1) direct measurements of the trees in the stand and 2) supplementary measurements of the stand area. The model is designed to start with a sample inventory of a stand. The compartment examination procedure described by Stage and Alley (1972) and in USDA Forest Service Handbook 2409.21h R1 (1986) can supply the necessary stand data. This should be augmented to include stumps infected with root disease.

The tree data often contain tree damage codes indicating individual trees as infected or located near infected trees. The timber inventory also can indicate sample plots with diseased trees or sample plots that are in diseased areas. If root disease occurs in clusters rather than in random centers within the stand, the tree inventory may miss or incorrectly represent its presence.

Supplementary measurements include an estimate of the total area of the stand with infected trees; the number of separate centers; the proportion of the trees in these centers that are infected; and, optionally, the location of individual centers. This information can be obtained from aerial photo interpretation (James et al. 1984) or from a special pest survey within the stand. Systematic survey methods such as transect lines with a fixed width are better able than a series of random plots to detect the presence of conditions that cluster within the stand (Bloomberg et al. 1980a).

Methods

Through model simulations of a sample stand and scrutinizing the survey data, the requirements of the model for data on initial disease conditions were examined. Limitations of the model in using detailed data on disease conditions were also examined.

In the following example, the stand's tree data are from an actual timber inventory. The stand's shape and the arrangement of the disease centers are contrived to illustrate points in the sampling and model simulation process. In figure 1, the general outline of stand 20257 is an irregular polygon (approximating a rectangle). Within this polygon are 10 root disease centers. The 10 lightly shaded circles represent reduced stand density in a root disease center. A series of seven smaller circles, connected by a line, represent the timber inventory plots. Note that two of the seven plots fall into root disease centers. The stand's size is 40 acres.

In simulating the stand, the Western Root Disease Model uses the timber inventory plot data. (Assume that aerial photos of the stand show that all 10 root disease centers were found and their combined area estimated.) These starting conditions were then supplied to the model. Figure 2 represents the model's view of the stand. The model assumes a square stand of equal area. The model will, by default, assign these 10 centers as circles of equal size located randomly unless location and size are supplied for each.

Stand projections with and without considering root disease lead to very different expectations in merchantable cubic volume for the stand over the next 150 years (fig. 3). The root disease model, like most pest models,

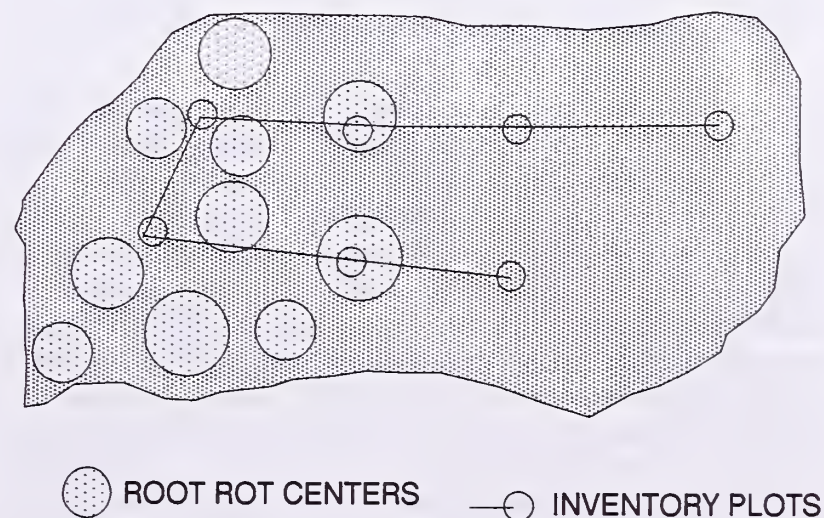


Figure 1.—A map of stand 20257 with location of inventory plots and root rot centers.

²Marsden, Michael A. 1992. *Sensitivity analyses of the Western Root Disease Model to user-specified starting parameters*. Res. Pap. RM-303. Fort Collins, CO: U.S. Department of Agriculture, Forest Service, Rocky Mountain Forest and Range Experiment Station. In review.

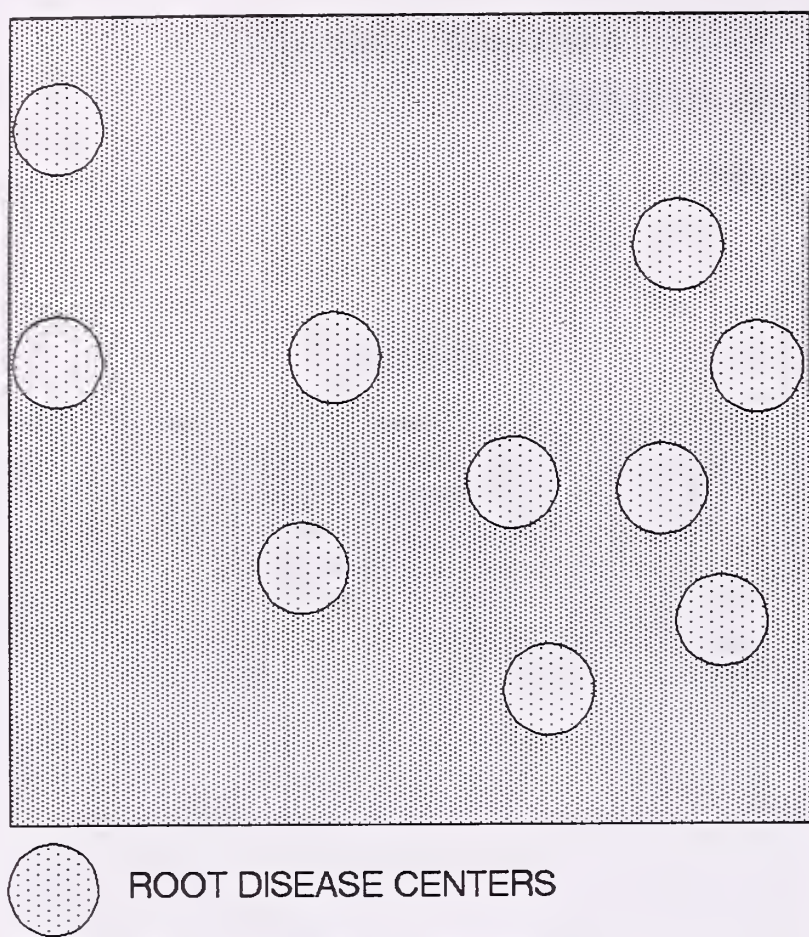


Figure 2.—The model's map of stand 20257 with random location of root rot centers.

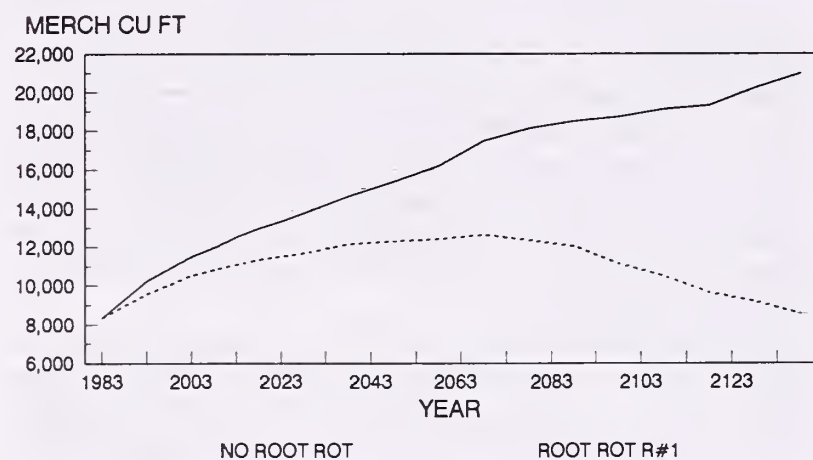


Figure 3.—Simulation of merchantable cubic foot volume for stand 20257: 1) without root rot, 2) with random root rot locations.

has a stochastic component. A second simulation (with a new starting value for the random component) will produce a slightly different result. To evaluate our stand, three simulations were made (fig. 4). Note that all three simulations with root disease predict a decline in volume after about 50–60 years. The rate of decline differs for each simulation. The major causes for the variation among these three simulations are the random placement of the 10 centers at the start and the random placement of trees within the centers. Other random components affect the simulations less.

The area with infected trees is directly related to the change in stand productivity. The area with disease is modeled to support little merchantable cubic foot volume compared with areas without infected trees. The

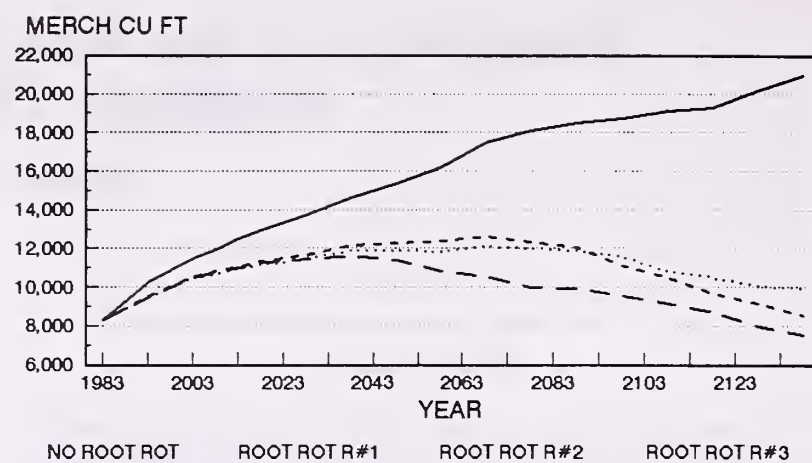


Figure 4.—Simulation of merchantable cubic foot volume for stand 20257: 1) without root rot, 2) with random root rot locations (3 replications).

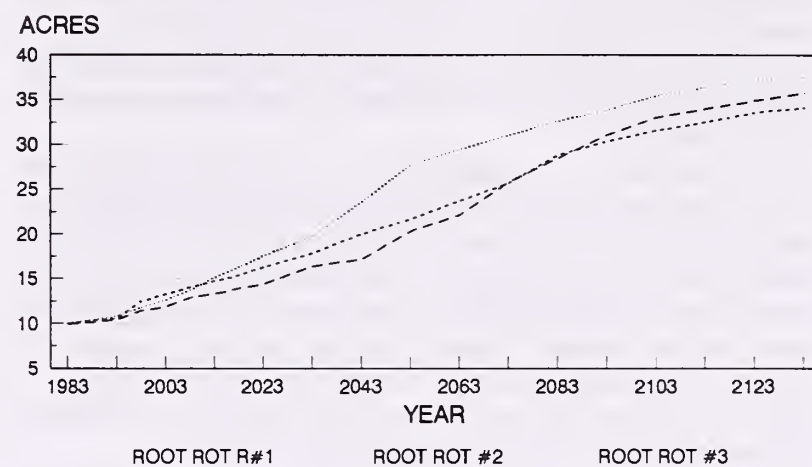


Figure 5.—Simulation of root rot center's area for stand 20257 with random root rot locations (3 replications).

area infected increases from 10 to 35 acres over a period of 140 years in the first simulation. Again, the three different simulations chart three different paths with respect to area infected (fig. 5). For the simulation of the "non-infected" stand, the area in the centers remains fixed at 10 acres and is not subject to greater mortality than the rest of the stand. The reduced stand density due to root disease serves only to lower the total stocking for the stand at the start of the simulation.

For our 40 acre stand to contain 35 acres in root disease centers at a future date is not likely if we consider the placement of the original 10 centers (fig. 1). Remember that the stand will be represented by a square in the model. But we could force the 10 root disease centers to be located in the left half of the stand, as depicted in figure 6. This configuration would more closely represent the assumed stand condition.

The difference due to this change in center distribution in simulating the impact of root disease is shown in figure 7. Again, the volume expected is less than in a noninfected stand, but far greater than expected under a random distribution of centers.

How will predictions vary for this fixed assignment of centers if we make repeated simulations with new random starts? Figure 8 shows that three fixed location simulations predict a stand of less cubic volume than did a prediction without root disease, yet more than the random location simulations. These differences are seen more clearly in the area with infected trees (fig. 9).

If we knew by prior inventory that root disease centers are located in one section of the stand more densely than in the other sections, we could stratify the stand into two components and simulate conditions in each separately. To do so correctly would require that we can stratify the timber inventory also.

Are the natural stands with root disease like the stand depicted in figure 1? Will random location of centers suffice for many stand simulations? While implementing a set of field trials to evaluate the utility of the line transect method for stands in the Rocky Mountains, we collected data that can also be used to answer these questions.

Root disease-infected stands on the Southern Ute Indian Reservation in Southwestern Colorado and on the Wallace Ranger District of the Idaho Panhandle National Forests were inventoried using the line transect sam-

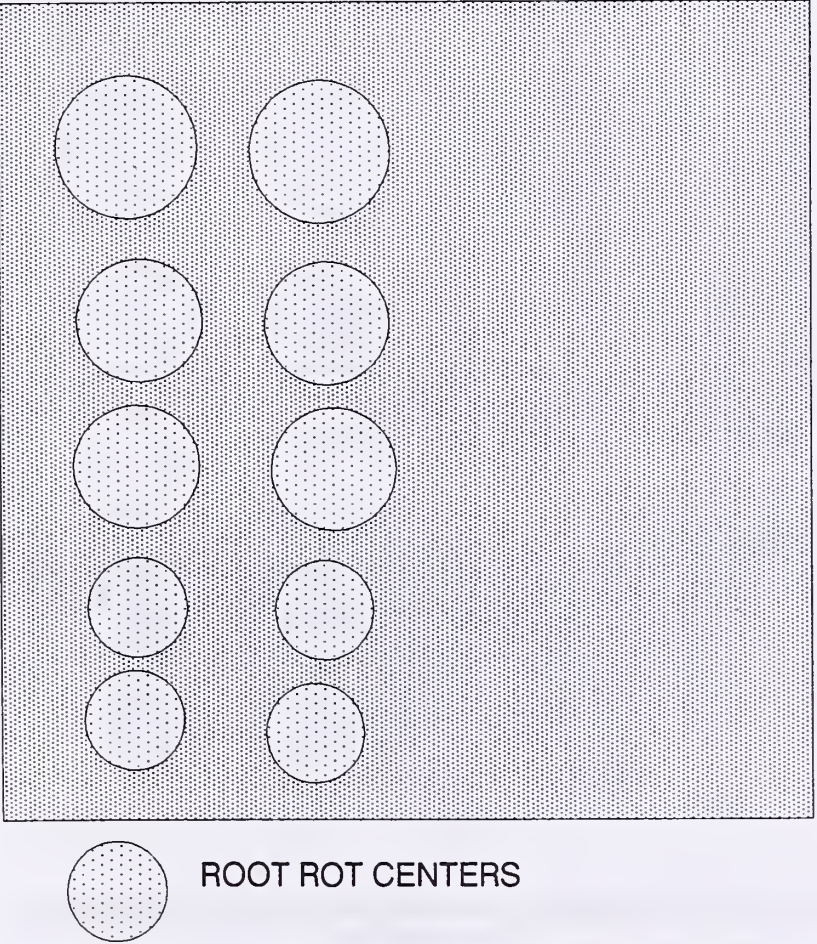


Figure 6.—The model's map of stand 20257 with fixed location of root rot centers.

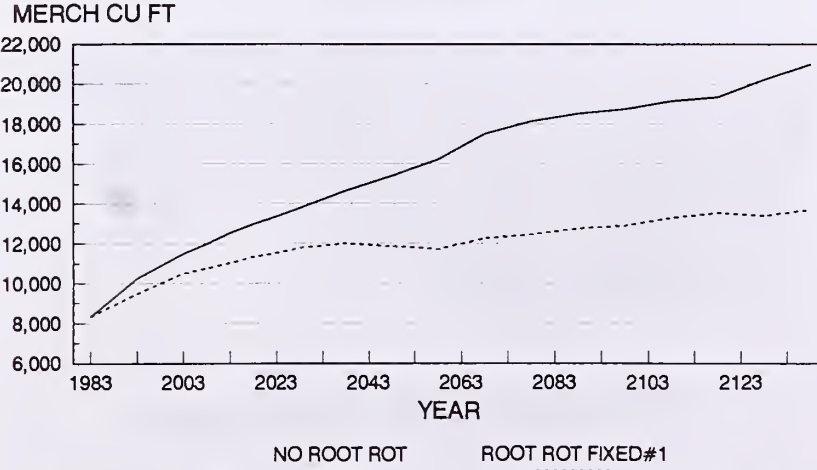


Figure 7.—Simulation of merchantable cubic foot volume for stand 20257: 1) without root rot, 2) with fixed root rot locations.

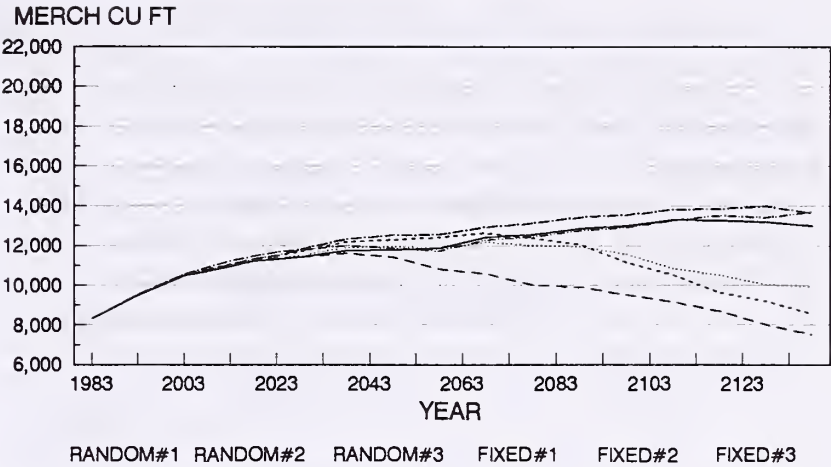


Figure 8.—Simulation of merchantable cubic foot volume for stand 20257: 1) with random root rot locations (3 replications), 2) with fixed root rot locations (3 replications).

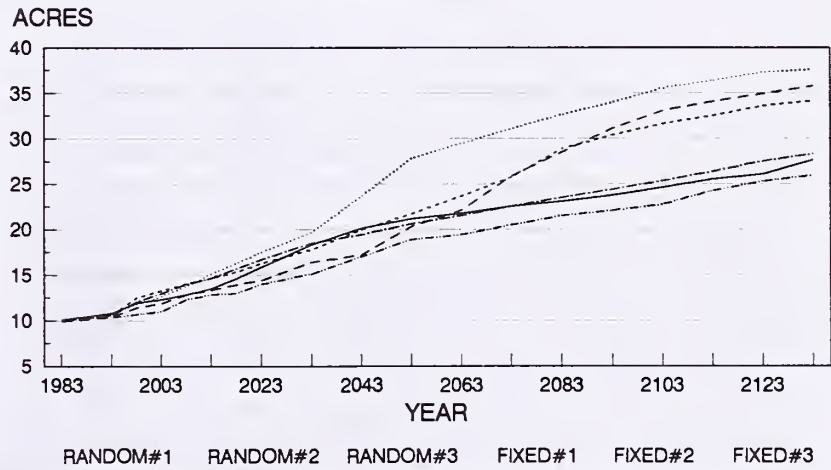


Figure 9.—Simulation of root rot center's area for stand 20257: 1) with random root rot locations (3 replications), 2) with fixed root rot locations (3 replications).

pling method (Bloomberg et al. 1980a, 1980b). Stands sampled in both Colorado and Idaho were naturally infected with *Armillaria*. Some were also infected with *Heterobasidion annosum*, which is not captured in the present model. The sampled stands in Colorado were ponderosa pine (*Pinus ponderosa*), sometimes with a large component of white fir (*Abies concolor*) and Douglas-fir (*Pseudotsuga menziesii*). Those in Idaho were mixed conifer stands with a larger component of Douglas-fir and grand fir (*Abies grandis*) plus several other species, including ponderosa pine and lodgepole pine (*Pinus contorta*). At each location we tried to pick stands with low to high levels of infection (table 1). We sampled stands with a level of infection of less than 1% to a high of over 50%. There were fewer than 10 centers in some stands. In stand 19303025, the number of disease centers is estimated at 104. Some stands in the Southern Ute Reservation had so much disease that individual centers were not measured. In these stands the percent of area with infected trees is estimated from the percent of the transect lines within disease locations. When a large portion of the stand has infected trees, the individual centers begin to overlap and lose their identity.

Through Bloomberg's intensive inventory techniques, we can collect the data needed to run a fixed location simulation for such stands. Two stands from table 1 were selected as examples in this study.

Table 1.—Stands on the Southern Ute Indian Reservation, Colorado, and the Wallace Ranger District, Idaho, surveyed for root disease.

Location	Year	Stand	Area (acres)	Estimated	
				Area with infected trees (percent)	Number of centers
Southern Ute	1990	06	41	1.4	28
		56	24	0.7	41
		89	7	2.9	10
	1991	9212-1	10	13.7	40
		9200-3	4	31.4	76 ^a
		9200-4	4	51.4	90 ^a
		11	30	4.3	28
		33	30	23.2	294 ^a
		87	10	6.0	43
		88	10	3.6	31
		99	10	0.6	6
		100	8	1.0	8
		118	27	0.6	14
Wallace R.D.	1990	11401011	10	6.9	19
		11401012	26	2.9	85
		11401019	13	4.1	10
		11401022	12	6.1	9
		11202013	21	0.9	26
		11401028	17	1.6	16
	1991	19303022	51	0.2	29
		19303026	47	1.2	70
		19303025	40	3.7	104
		19303031	20	2.3	40
		19303033	2	1.2	60

^aRoot disease centers may overlap; total number of centers is poorly estimated as a result.

Stands 11401011 and 11401028 both occur on the Wallace Ranger District. These stands were inventoried using a series of transect lines following the method described by Bloomberg et al. (1980b). A series of three grids was imposed on the area; each grid had four transect lines and a random start. One side of the stand was a straight line—the baseline for the transect lines. The transect lines were 30 feet wide and perpendicular to the baseline (fig. 10). Any tree or group of trees with root disease along the transect is mapped as a center even if it contained only one symptomatic tree (fig. 11).

Even with these sparse data, the root disease is shown to be more dense in the left half of the stand. Since the transect lines are only 30 feet wide and the distance between transect lines on the same grid is much greater, disease centers found may represent only a fraction of the total number of centers in the stand.

The probability of detection for the i^{th} root disease center is

$$P_i = (D_i + W)/T, \text{ where}$$

D_i = diameter of the i^{th} center

W = width of the transect

T = distance between transect lines

The total stand area with root disease, T_d , and total number of centers, T_n , can be estimated as the weighted sum of the areas, A_i , of the sampled centers:

$$T_d = \sum A_i/P_i$$

$$T_n = \sum 1/P_i$$

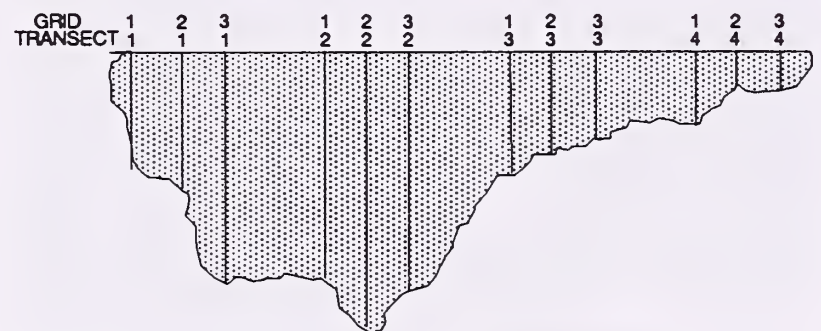


Figure 10.—A map of stand 11401028, Wallace R.D., with transect line locations.

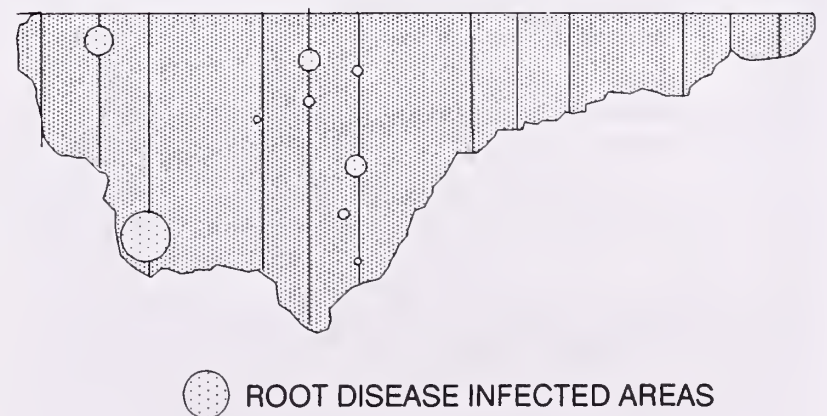


Figure 11.—A map of stand 11401028, Wallace R.D., with transection lines and sample root rot center locations.

Totals are calculated separately for each grid, then averaged. For irregular-shaped stands, the total transect lengths may differ among the three grids. The totals can be weighted by total transect length per grid and a weighted average computed for improved precision.

For stand 11401028 the estimate is 16 centers, which is 8 more centers than were on the transect lines. We estimated that one of these centers would be very large, one mid-size and the other six small. The additional root disease centers are distributed, with judgment, near the other centers of the same size, but not on a transect line (fig. 12). Here we must admit that our placement of the additional eight centers can enhance or decrease the degree of root disease clustering within the stand.

Although this figure resembles the constructed example at the beginning (fig. 1), the density of area with infected trees is much less in this stand (fig. 12). There is no need to worry if centers overlap in the simulation of this stand. Sufficient space exists for expanding the centers without overlap. A random placement of centers for the simulation would be approximate to actual stand conditions even though these centers appear clustered.

The second stand, 11401011, is shown in figure 13. Again, three grids with four transect lines each are used to inventory the stand. Only six root disease areas are found, but four are large. Most importantly, three of these lie very close to each other. If we place the total expected number of root disease areas on the stand and let them cluster as the sample centers do, we have the

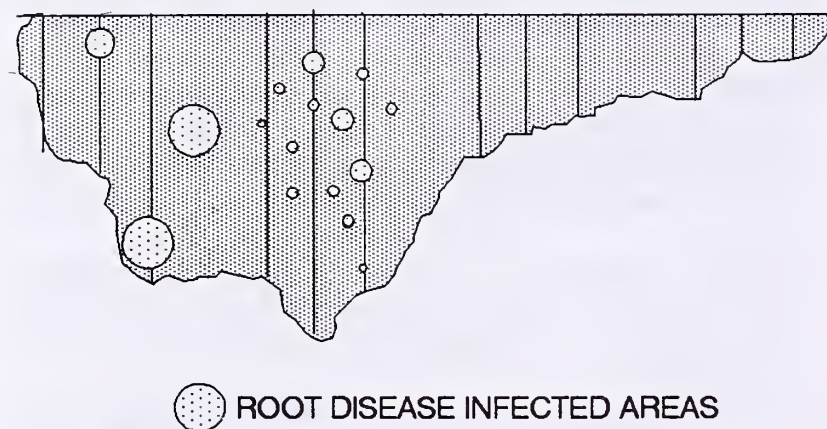


Figure 12.—A map of stand 11401028, Wallace R.D., with transect lines and total estimated root rot center locations.

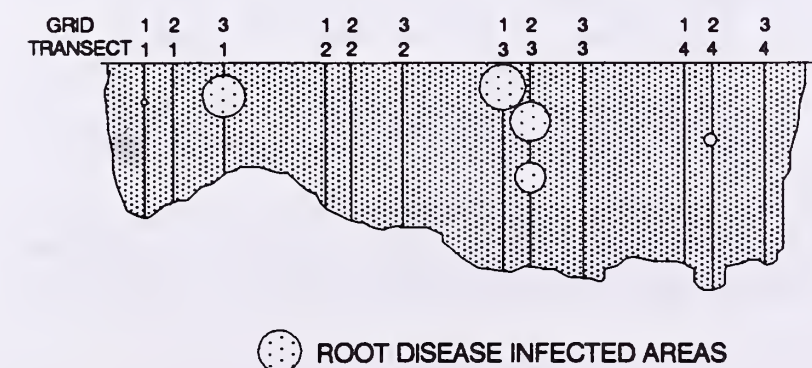


Figure 13.—A map of stand 11401011, Wallace R.D., with transect lines and sample root rot center locations.

potential for overlap (fig. 14). For long-term simulations (50–100 years), the overlap of these centers could alter the predicted timber volume. The random placement of centers is not recommended for this stand simulation.

In our first example, stand 20257, we showed the difficulty of stipulating the size and location of each center and the limitation of the model to use such information. For stand 11401028, a random assignment of root disease centers was sufficient to model the stand. For the last stand the total area with diseased trees is not great, but the disease centers are clustered. Stand 11401011 could be divided into four sections as indicated by the inventory method (fig. 15). Sections one, two, and four could be simulated as a single stand and section three as a separate stand with greater density of root disease. Following simulation the two stands could be combined. Since the simulation need not be concerned with the root disease spreading from section three into sections two and four, this would be sufficient.

When modeling a stand with 10 or fewer root disease centers, the model can be very sensitive to the number of centers. The effect of the disease area being modeled as 2 or 10 centers is significant.² Locating centers with respect to one another can be important as shown here in comparing fixed versus random location of centers. However, it is less likely when the number of centers is 20 or more that one would use fixed center locations. The maximum number of centers the model can simulate is 100. If the stand has many disease centers or the

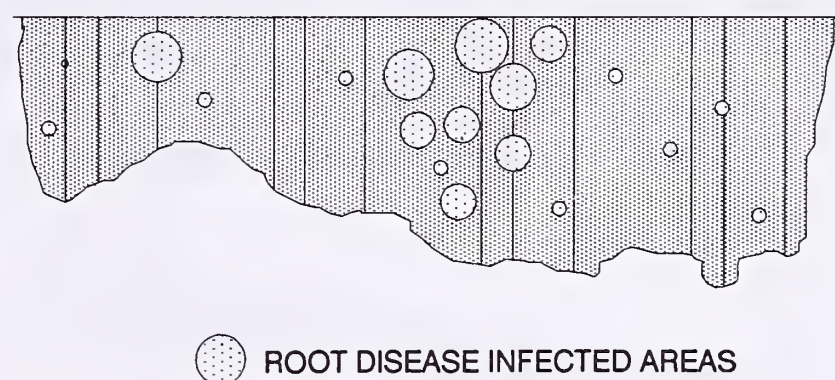


Figure 14.—A map of stand 11401011, Wallace R.D., with transect lines and total estimated root rot center locations.

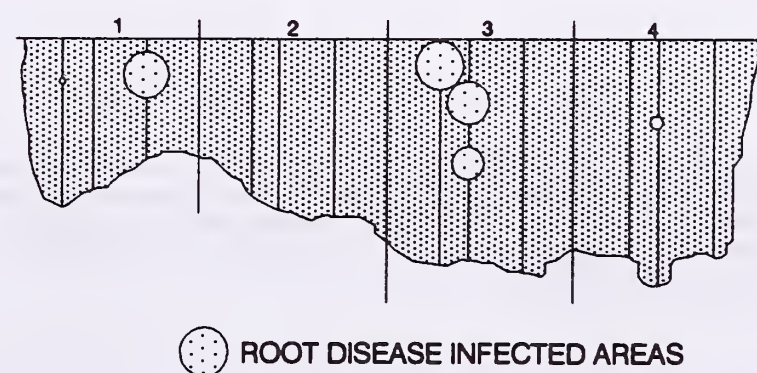


Figure 15.—A map of stand 11401011, Wallace R.D., divided into four sections with transect lines and sample root rot center locations.

definition of individual centers is blurred, it can be modeled as one center with the area equal to the stand area.

In general, if the initial area with infected trees and proportion of trees infected are held constant, the decrease in simulated volume will be greater when the initial number of centers is greater. This is shown in the next set of simulations that begin with the same starting conditions except for number of centers (fig. 16). Number of centers is set at 1, 5, 10, 20, 40, 60, and 100. Note that the set with 10 centers is the model's default starting conditions. For this set of starting conditions, merchantable volume is projected to be the least when the number of centers is 100.

If we model the entire stand as one disease center, the merchantable volume is still less (fig. 16). In this last simulation the initial proportion of trees infected is reduced so the number of infected trees at the start is approximately the same as for the other simulations. On the other runs of the model the proportion of infected trees is measured on 25 acres; for the last simulation the proportion is measured over the entire 100 acres.

Discussion and Conclusions

In using the Western Root Disease Model, consider the following points. The timber inventory system may not be sufficient to estimate the number, size, or distribution of root disease centers within a stand. The timber inventory data can be supplemented with information from such sources as aerial photo interpretation or a new disease inventory. The system of transect lines developed by Bloomberg can potentially provide all the additional information the model can use to construct a simulation of the diseased stand. The number, size, and distribution of root disease centers affect the stand

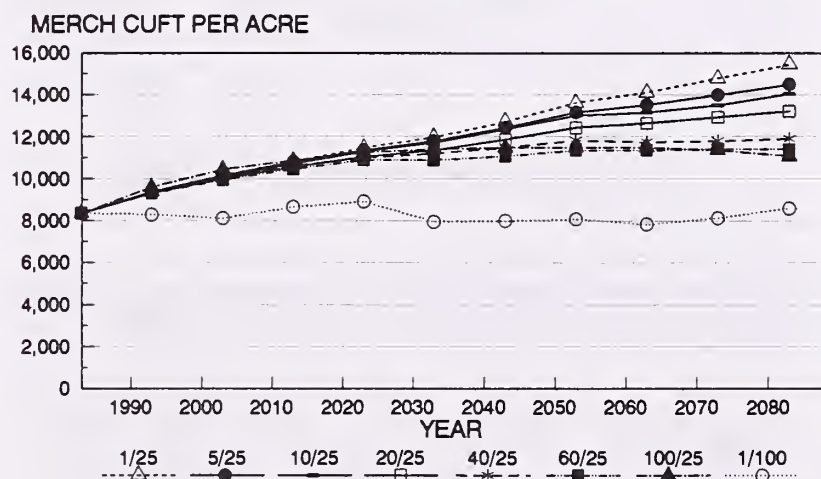


Figure 16.—Simulations of merchantable cubic foot volume for stand 20257 with eight levels of initial root rot infection indexed by ratio (number of centers/area infected). All simulations have 50% of trees in centers infected except (1/100), which has 12.5% of trees in the stand infected.

projection. Due to model limitations, detailed location and inventory of each root disease center is not productive. To use the model, it will often be sufficient to partition the stand into units in which root disease is randomly assigned a location.

The transect inventory system could be conducted when root disease is detected in the timber inventory with the resulting transect data analyses used to partition the stand into homogenous units with respect to disease density. Within such units, root disease could be modeled as occurring at random. Detailed simulation of a given stand is constrained because the model uses a square area to represent the actual stand. Long range simulations can exceed the capability of the model's spatial resolution.

The partition of the stand often will not be consistent with the assumptions for the timber inventory. This could lead to biased estimates for the entire stand. If the locations of the timber inventory points are known, it may be possible to post-stratify this inventory based on how one divides the stand for root disease conditions.

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Marsden, Michael A. 1992. Sensitivity of the Western Root Disease Model: Inventory of root disease. Res. Pap. RM-303. Fort Collins, CO: U.S. Department of Agriculture, Forest Service, Rocky Mountain Forest and Range Experiment Station. 6 p.

The Western Root Disease Model can be used to simulate the spread and impact of *Armillaria* spp. and *Phellinus weirii* (Murr.[Gilbn.]) in western coniferous forests. The simulations are sensitive to the information on initial disease conditions supplied to the model. Forest inventory requirements and model limitations are demonstrated.

Keywords: *Armillaria*, *Phellinus weirii*, Prognosis Model, disease impact, root rot



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Rocky Mountain Forest and Range Experiment Station

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